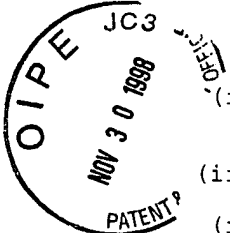


SEQUENCE LISTING

#8/C

(1) GENERAL INFORMATION:

- (i) APPLICANT: KAYAGAKI, Nobuhiko
YAGITA, Kideo
OKUMURA, Ko
NAKATA, Motomi
- (ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: McDermott, Will & Emery
(B) STREET: 99 Canal Center Plaza, Suite 300
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: USA
(F) ZIP: 22314
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/913,555
(B) FILING DATE: 19-SEP-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Bucca Ph.D., Daniel
(B) REGISTRATION NUMBER: 42,368
(C) REFERENCE/DOCKET NUMBER: 50356-150
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-756-8600
(B) TELEFAX: 202-756-8699



(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Glu | Leu | Val | Lys | Pro | Gly | Ala | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ala | Phe | Ser | Ser | Trp | |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Met | Asn | Trp | Val | Lys | Gln | Arg | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Ile | Gly |
| | | | 35 | | | | | 40 | | | | | 45 | | |

Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys
50 55 60

Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
65 70 75 80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala
85 90 95

Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCAGCTGC AGGAGTCTGG ACCTGAGCTG GTGAAGCCTG GGCCTCAGT GAAGATTTCC	60
TGCAAGGCTT CTGGCTATGC ATTCAGTAGC TCCTGGATGA ACTGGGTGAA GCAGAGGCCT	120
GGAAAGGGTC TTGAGTGGAT TGGACGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC	180
GGGAAGTTCA AGGGCAAGGC CAACTGACC GCAGACAAAT CCTCCAGCAC AGCCTACATG	240
CAACTCAGCA GTCTGACATC TGAGGACTCT GCGGTCTACT TCTGTGCAAG ATCGTATTAC	300
TACGATGGTA GCCCCTGGTT TACTTACTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA	360

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACATCCAGA TGACGCAGTC TCCATCCTCC CTGTCTGCCT CTCTGGGAGA CAGAGTCACC	60
ATCAGTTGCA GGGCAAGTCA GGATATTAGC AATTATTTAA ACTGGTATCA GCAGAAACCA	120
GATGGAAGTCT TAAACTCCT GATCTACTAC ACATCAAGAT TAACTCAGG AGTCCCATCA	180
AGGTTCAAGTGC GAGTGGGTC TGGGACAGAT TATTCTCTCA CCATCAGCAA CCTGGAACCT	240
GAAGATATTG CCACTTACTT TTGTCAGCAA TATAGTGAAT TTCCGTGGAC GTTCGGTGA	300
GGCACCAAGC TGGAAATCAA ACGG	324

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr Ser
 1 5 10 15
 Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asn Tyr Trp
 20 25 30
 Ile Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly
 35 40 45
 Tyr Leu Tyr Pro Gly Gly Leu Tyr Thr Asn Tyr Asn Glu Lys Phe Lys
 50 55 60
 Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met

65		70		75		80									
Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Ile	Tyr	Tyr	Cys	Ala
			85						90					95	
Arg	Tyr	Arg	Asp	Tyr	Asp	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Thr	Val	Thr	Val	Ser	Ser										
			115												

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGCAGCTGC AGCAGTCAGG AGCTGAGCTG GTAAGGCCTG GGACTTCAGT GAAGATGTCC	60
TGCAAGGCTG CTGGATACAC CTTCACTAAC TACTGGATAG GTTGGGTAAA GCAGAGGCCT	120
GGACATGGCC TTGAGTGGAT TGGATATCTT TACCCTGGAG GTCTTTATAC TAACTACAAT	180
GAGAAGTTCA AGGGCAAGGC CACACTGACT GCAGACACAT CCTCCAGCAC AGCCTACATG	240
CAGCTCAGCA GCCTGACATC TGAGGACTCT GCCATCTATT ACTGTGCAAG ATACAGGGAT	300
TACGACTATG CTATGGACTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCA	354

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp	Val	Leu	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Asn	Ile	Gly
1				5				10					15		
Asp	Gln	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Thr	Lys	Ser	Leu	Leu	Asn	Ser
		20					25					30			
Asp	Gly	Phe	Thr	Tyr	Leu	Gly	Trp	Cys	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35				40					45				
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro
	50					55				60					
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65					70					75				80	

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser
85 90 95

Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATGTTTGA TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTCT	60
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACTTA TTTGGGCTGG	120
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATTT	180
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTAC CCTCAAGATC	240
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCCT	300
CTTACGTTTC GATCGGGGAC CAAGCTGGAA ATAAACGG	339

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser	1 5 10 15
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser Trp	20 25 30
Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly	35 40 45
Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys	50 55 60
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met	65 70 75 80
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala	

[illegible]

Val Tyr Tyr Tyr Asp Gly Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGCAGCTGC AGGAGTCTGG ACCTGGCCTC GTGAAACCTT CTCAGTCTCT GTCTCTCACC	60
TGCTCTGTCA CTGGCTACTC CATCACCAGT GGTATTACT GGAAGTGGAT CCGGCAGTTT	120
CCAGGAAACA AACTGGAATG GATGGGCTAC ATAAGCTACG ATGGTAGCAA TAACTACAAC	180
CCATCTCTCA AAAATCGAAT CTCCATCACT CGTGACACAT CTAAGAACCA GTTTTTCTCTG	240
AAGTTGAATT CTGTGACTAC TGAGGACACA GCCACATATT ACTGTGCCGT TTATTACTAC	300
GATGGTAGCT CTTTGTACTA CTGGGGCCAA GGGACCACGG TCACCGTCTC CTCA	354

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Arg	1 5 10 15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Gly Val Asp Ser Tyr	20 25 30
Gly Ile Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro	35 40 45
Lys Leu Leu Ile Tyr Arg Ala Ser Tyr Leu Lys Ser Gly Val Pro Ala	50 55 60
Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp	65 70 75 80
Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn	85 90 95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GACATTGTGC TGACCCAATC TCCAGCTTCT TTGGCTGTGT CTCTAAGGCA GAGGGCCACC      60
ATATCCTGCA GAGCCAGTGA AGGTGTTGAT AGTTATGGCA TTAGTTTTAT GCACTGGTAC      120
CAGCAGAAAC CAGGACAGCC ACCCAAATC CTCATCTATC GTGCATCCTA CCTAAAATCT      180
GGGGTCCCTG CCAGGTTTCTG TGGTAGTGGG TCTAGGACAG ACTTCACCCT CACCATTGAT      240
CCTGTGGAGG CTGATGATGC TGCAACCTAT TACTGTGACG AAAATAATGA GGATCCGTGG      300
ACGTTCGGTG GAGGCACCAA GCTGGAAATC AAACGG                                336

```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Val Gln Leu Gln Glu Ser Gly Ala Glu Pro Ala Lys Pro Gly Ala Ser
1           5           10           15
Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr Trp
20          25          30
Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
35          40          45
Tyr Ile Asn Pro Ser Ser Gly Tyr Thr Glu Tyr Asn Gln Lys Phe Lys
50          55          60
Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
65          70          75          80
Gln Leu Ile Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
85          90          95
Arg Arg Gly Asn Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100         105         110
Val Thr Val Ser Ser

```


(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTGCAGCTGC AGGAGTCTGG GGCTGAACCG GCAAAACCTG GGGCCTCAGT GAAGATGTCC      60
TGCAAGGCTT CTGGCTACAC CTTTACTACC TACTGGATGC ACTGGGTAAA ACAGAGGCCT      120
GGACAGGGTC TGAATGGAT TGGATACATT AATCCTAGCA GTGGTTATAC TGAGTACAAT      180
CAGAAGTTCA AGGACAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG      240
CAACTAATCA GCCTGACATC TGAGGACTCT GCAGTCTATT ACTGTGCAAG AAGGGGTAAT      300
TACTACTACT TTGACTACTG GGGCCAAGGG ACCACGGTCA CCGTCTCCTC A              351

```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Asp Val Leu Met Thr Gln Thr Pro Lys Phe Leu Pro Val Ser Ala Gly
1           5           10           15
Asp Arg Val Thr Met Thr Cys Lys Ala Ser Gln Ser Val Gly Asn Asn
20        25        30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35        40        45
Tyr Tyr Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50        55        60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Val
65        70        75        80
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr Ser Ser Pro Tyr
85        90        95
Thr Phe Gly Ser Gly Thr Lys Leu Glu
100       105

```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGTTTGA TGACCCAAAC TCCAAAATTC CTGCCTGTAT CAGCAGGAGA CAGGGTTACC	60
ATGACCTGCA AGGCCAGTCA GAGTGTGGGT AATAATGTGG CCTGGTACCA ACAGAAGCCA	120
GGACAGTCTC CTAAACTGCT GATATACTAT ACATCCAATC GCTACACTGG AGTCCCTGAT	180
CGCTTCACTG GCAGTGGATC TGGGACAGAT TTCACCTTCA CCATCAGCAG TGTGCAGGTT	240
GAAGACCTGG CAGTTTATTT CTGTCAGCAG CATTATAGCT CTCCGTATAC GTTCGGATCG	300
GGGACCAAGC TGGAG	315

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala	1	5	10	15
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser	20	25	30	
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile	35	40	45	
Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe	50	55	60	
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	65	70	75	80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys	85	90	95	
Ala Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly	100	105	110	
Gln Gly Thr Leu Val Thr Val Ser Ala	115	120		

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGGTTTCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCCTC AGTGAAGATT	60
TCCTGCAAGG CTTCTGGCTA TGCATTCACT AGCTCCTGGA TGAAGTGGGT GAAGCAGAGG	120
CCTGGAAGG GTCTTGAGTG GATTCGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC	180
GGGAAGTTCA AGGGAGGCAA GGCCACACTG ACCGCAGACA AATCCTCCAG CACAGCCTAC	240
ATGCAACTCA GCAGTCTGAC ATCTGAGGAC TCTGCGGTCT ACTTCTGTGC AAGATCGTAT	300
TACTACGATG GTAGCCCCTG GTTTACTTAC TGGGGCCAAG GGACTCTGGT CACTGTCTCT	360
GCA	363

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly	
1 5 10 15	
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr	
20 25 30	
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile	
35 40 45	
Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly	
50 55 60	
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro	
65 70 75 80	
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Glu Phe Pro Trp	
85 90 95	
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	
100 105	

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid

(ii) MOLECULE TYPE: cDNA to mRNA

GATATCCAGA	TGACACAGAC	TACATCCTCC	CTGTCTGCCT	CTCTGGGAGA	CAGAGTCACC	60
ATCAGTTGCA	GGGCAAGTCA	GGATATTAGC	AATTATTTAA	ACTGGTATCA	GCAGAAACCA	120
GATGGAACTG	TTAAACTCCT	GATCTACTAC	ACATCAAGAT	TACACTCAGG	AGTCCCATCA	180
AGGTTCAAGT	GCAGTGGGTC	TGGGACAGAT	TATTCTCTCA	CCATCAGCAA	CCTGGAACCT	240
GAAGATATTG	CCACTTACTT	TTGTCAGCAA	TATAGTGAAT	TTCCGTGGAC	GTTCGGTGGA	300
GGCACCAAGC	TGGAAATCAA	ACGG				324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(ii) MOLECULE TYPE: cDNA to mRNA

CAGGTCCACC	TGCAGCAGTC	TGGAGCTGAG	CTGGTAAGGC	CTGGGACTTC	AGTGAAGATG	60
TCCTGCAAGG	CTGCTGGATA	CACCTTCACT	AACTACTGGA	TAGGTTGGGT	AAAGCAGAGG	120
CCTGGACATG	GCCTTGAGTG	GATTGGATAT	CTTTACCCTG	GAGGTCTTTA	TACTAACTAC	180
AATGAGAAGT	TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	CATCCTCCAG	CACAGCCTAC	240
ATGCAGCTCA	GCAGCCTGAC	ATCTGAGGAC	TCTGCCATCT	ATTACTGTGC	AAGATACAGG	300
GATTACGACT	ATGCTATGGA	CTACTGGGGT	CAAGGAACCT	CAGTCAACCGT	CTCCTCA	357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATGTTGTTC TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTCT	60
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACCTA TTTGGGCTGG	120
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATTT	180
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTTAC CCTCAAGATC	240
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCCT	300
CTTACGTTTCG GATCGGGGAC CAAGCTGGAA ATAAAACGG	339

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala	15
1 5 10	
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser	30
20 25 30	
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile	45
35 40 45	
Gly Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe	60
50 55 60	
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	80
65 70 75 80	
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys	95
85 90 95	
Ala Thr Asp Gly Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr	110
100 105 110	
Val Thr Val Ser Ser	115

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGTCAGC TGCAGCAGTC TGGACCTGAG CTGGTGAAGC CTGGGGCCTC AGTGAAGATT	60
TCCTGCAAGG CTTCTGGCTA TGCATTCAGT AGCTCCTGGA TGAAGTGGGT GAAACAGAGG	120
CCTGGGAAGG GTCTTGAGTG GATTGGACGG ATTTATCCTG TAAATGGAGA TACTAACTAC	180
AATGGGAAGT TCAAGGGCAA GGCCACACTG ACTGCAGACA AATCCTCCAG CACAGCCTAC	240
ATGCAACTCA GCAGCCTGAC ATCTGAGGAC TCTGCGGTCT ACTTCTGTGC AACCGATGGT	300
TACTGGTACT TCGATGTCTG GGGCGCAGGG ACCACGGTCA CCGTCTCCTC A	351

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly	
1 5 10 15	
Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ile Tyr	
20 25 30	
Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile	
35 40 45	
Tyr Gly Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly	
50 55 60	
Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ala	
65 70 75 80	
Glu Asp Leu Ser Asp Tyr Tyr Cys Val Gln Ser Tyr Ser Tyr Pro Trp	
85 90 95	
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg	
100 105	

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGAGCTGCA AGGCCAGTGA GAATGTGGAT ATTTATGTAT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATACGGG ACATCCAACC GGTACACTGG GGTCCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAA TGTGCAGGCT	240
GAAGACCTTT CAGATTATTA CTGTGTACAG AGTTACAGCT ATCCGTGGAC ATTCGGTGGA	300
GGCACCAAGC TGGAAATCAA ACGG	324

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu	Ser	His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln
1				5					10				